E. O'Hara (signature)

ENTERED

1600

#/2

RAW SEQUENCE LISTING
PATENT APPLICATION: **US/09/899,422A**

DATE: 08/27/2003
TIME: 12:54:43

Input Set : **N:\EBONY'S\US09899422A.raw.txt**
Output Set: **N:\CRF4\08272003\I899422A.raw**

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      1 <110> APPLICANT: Hauptmann, Rudolph
      2         Himmler, Adolph
      3         Maurer-Fogy, Ingrid
      4         Stratowa, Christian
      5 <120> TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
      6         Them
      7 <130> FILE REFERENCE: 98-385-H
C-->  8 <140> CURRENT APPLICATION NUMBER: US/09/899,422A
      9 <141> CURRENT FILING DATE: 2001-07-03·
     10 <150> PRIOR APPLICATION NUMBER: 09/525,998
     11 <151> PRIOR FILING DATE: 2000-03-15
     12 <150> PRIOR APPLICATION NUMBER: 08/383,676
     13 <151> PRIOR FILING DATE: 1995-02-01
     14 <150> PRIOR APPLICATION NUMBER: 08/153,287
     15 <151> PRIOR FILING DATE: 1993-11-17
     16 <150> PRIOR APPLICATION NUMBER: 07/821,750
     17 <151> PRIOR FILING DATE: 1992-01-02
     18 <150> PRIOR APPLICATION NUMBER: 07/511,430
     19 <151> PRIOR FILING DATE: 1990-04-20
     20 <160> NUMBER OF SEQ ID NOS: 97
     21 <170> SOFTWARE: PatentIn Ver. 2.0
     23 <210> SEQ ID NO: 1
     24 <211> LENGTH: 1368
     25 <212> TYPE: DNA
     26 <213> ORGANISM: Homo sapiens
     27 <220> FEATURE:
     28 <221> NAME/KEY: CDS
     29 <222> LOCATION: (1)..(1365)
     30 <220> FEATURE:
     31 <221> NAME/KEY: sig_peptide
     32 <222> LOCATION: (1)..(87)
     33 <220> FEATURE:
     34 <221> NAME/KEY: misc_feature
     35 <222> LOCATION: (88)..(120)
     36 <223> OTHER INFORMATION: portion of TNF-BP pro protein cleaved by
     37         extracellular proteases following secretion
     38 <220> FEATURE:
     39 <221> NAME/KEY: misc_feature
     40 <222> LOCATION: (606)..(633)
     41 <223> OTHER INFORMATION: portion of TNF-BP pro protein cleaved by
     42         extracellular proteases following secretion
     43 <400> SEQUENCE: 1
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45        Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro Leu Val Leu Leu
46         1               5                  10                  15
47        gag ctg ttg gtg gga ata tac ccc tca ggg gtt att gga ctg gtc cct    96
48        Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu Val Pro
49                        20                  25                  30
50        cac cta ggg gac agg gag aag aga gat agt gtg tgt ccc caa gga aaa   144
51        His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys
52                    35                  40                  45
53        tat atc cac cct caa aat aat tcg att tgc tgt acc aag tgc cac aaa   192
54        Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys
55              50                  55                  60
56        gga acc tac ttg tac aat gac tgt cca ggc ccg ggg cag gat acg gac   240
57        Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp
58           65                  70                  75                  80
59        tgc agg gag tgt gag agc ggc tcc ttc acc gct tca gaa aac cac ctc   288
60        Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu
61                        85                  90                  95
62        aga cac tgc ctc agc tgc tcc aaa tgc cga aag gaa atg ggt cag gtg   336
63        Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val
64                    100                 105                 110
65        gag atc tct tct tgc aca gtg gac cgg gac acc gtg tgt ggc tgc agg   384
66        Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg
67                    115                 120                 125
68        aag aac cag tac cgg cat tat tgg agt gaa aac ctt ttc cag tgc ttc   432
69        Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe
70              130                 135                 140
71        aat tgc agc ctc tgc ctc aat ggg acc gtg cac ctc tcc tgc cag gag   480
72        Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu
73           145                 150                 155                 160
74        aaa cag aac acc gtg tgc acc tgc cat gca ggt ttc ttt cta aga gaa   528
75        Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu
76                    165                 170                 175
77        aac gag tgt gtc tcc tgt agt aac tgt aag aaa agc ctg gag tgc acg   576
78        Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr
79                    180                 185                 190
80        aag ttg tgc cta ccc cag att gag aat gtt aag ggc act gag gac tca   624
81        Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser
82                    195                 200                 205
83        ggc acc aca gtg ctg ttg ccc ctg gtc att ttc ttt ggt ctt tgc ctt   672
84        Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu
85              210                 215                 220
86        tta tcc ctc ctc ttc att ggt tta atg tat cgc tac caa cgg tgg aag   720
87        Leu Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys
88         225                 230                 235                 240
89        tcc aag ctc tac tcc att gtt tgt ggg aaa tcg aca cct gaa aaa gag   768
90        Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys Glu
91                    245                 250                 255
92        ggg gag ctt gaa gga act act act aag ccc ctg gcc cca aac cca agc   816
93        Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser
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RAW SEQUENCE LISTING   DATE: 08/27/2003
PATENT APPLICATION: **US/09/899,422A**   TIME: 12:54:43

Input Set : **N:\EBONY'S\US09899422A.raw.txt**
Output Set: **N:\CRF4\08272003\I899422A.raw**

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94                  260              265              270
95      ttc agt ccc act cca ggc ttc acc ccc acc ctg ggc ttc agt ccc gtg   864
96      Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe Ser Pro Val
97·             275              280              285
98      ccc agt tcc acc ttc acc tcc agc tcc acc tat acc ccc ggt gac tgt   912
99      Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr Pro Gly Asp Cys
100            290              295              300
101     ccc aac ttt gcg gct ccc cgc aga gag gtg gca cca ccc tat cag ggg   960
102     Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro Pro Tyr Gln Gly
103     305                  310              315                  320
104     gct gac ccc atc ctt gcg aca gcc ctc gcc tcc gac ccc atc ccc aac   1008
105     Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp Pro Ile Pro Asn
106            325              330              335
107     ccc ctt cag aag tgg gag gac agc gcc cac aag cca cag agc cta gac   1056
108     Pro Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro Gln Ser Leu Asp
109            340              345              350
110     act gat gac ccc gcg acg ctg tac gcc gtg gtg gag aac gtg ccc ccg   1104
111     Thr Asp Asp Pro Ala Thr Leu Tyr Ala Val Val Glu Asn Val Pro Pro
112            355              360              365
113     ttg cgc tgg aag gaa ttc gtg cgg cgc cta ggg ctg agc gac cac gag   1152
114     Leu Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu Ser Asp His Glu
115     370                  375              380
116     atc gat cgg ctg gag ctg cag aac ggg cgc tgc ctg cgc gag gcg caa   1200
117     Ile Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln
118     385                  390              395                  400
119     tac agc atg ctg gcg acc tgg agg cgg cgc acg ccg cgg cgc gag gcc   1248
120     Tyr Ser Met Leu Ala Thr Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala
121            405              410              415
122     acg ctg gag ctg ctg gga cgc gtg ctc cgc gac atg gac ctg ctg ggc   1296
123     Thr Leu Glu Leu Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly
124            420              425              430
125     tgc ctg gag gac atc gag gag gcg ctt tgc ggc ccc gcc gcc ctc ccg   1344
126     Cys Leu Glu Asp Ile Glu Glu Ala Leu Cys Gly Pro Ala Ala Leu Pro
127            435              440              445
128     ccc gcg ccc agt ctt ctc aga tga                                   1368
129     Pro Ala Pro Ser Leu Leu Arg
130            450              455
132 <210> SEQ ID NO: 2
133 <211> LENGTH: 455
134 <212> TYPE: PRT
135 <213> ORGANISM: Homo sapiens
136 <400> SEQUENCE: 2
137     Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro Leu Val Leu Leu
138      1               5               10                  15
139     Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu Val Pro
140            20              25                  30
141     His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys
142            35              40              45
143     Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys
```

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144              50                    55                    60
145     Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp
146      65                  70                  75                  80
147     Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu
148                      85                  90                  95
149     Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val
150                 100                 105                 110
151     Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg
152                 115                 120                 125
153     Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe
154             130                 135                 140
155     Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu
156     145                 150                 155                 160
157     Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu
158                 165                 ·      170                 175
159     Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr
160                 180                 185                 190
161     Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser
162                 195                 200                 205
163     Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu
164             210                 215                 220
165     Leu Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys
166     225                 230                 235                 240
167     Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys Glu
168                 245  ,              250                 255
169     Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser
170                 260                 265                 270
171     Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe Ser Pro Val
172                 275                 280                 285
173     Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr Pro Gly Asp Cys
174             290                 295                 300
175     Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro Pro Tyr Gln Gly
176     305                 ·310                 315                 320
177     Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp Pro Ile Pro Asn
178                 325                 330                 ·335
179     Pro Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro Gln Ser Leu Asp
180             340                 345                 350
181     Thr Asp Asp Pro Ala Thr Leu Tyr Ala Val Val Glu Asn Val Pro Pro
182             355                 360                 365
183     Leu Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu Ser Asp His Glu
184         370                 375                 380
185     Ile Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln
186     385                 390                 395                 400
187     Tyr Ser Met Leu Ala Thr Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala
188             405                 410                 415
189     Thr Leu Glu Leu Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly
190             420                 425                 430
191     Cys Leu Glu Asp Ile Glu Glu Ala Leu Cys Gly Pro Ala Ala Leu Pro
192             435                 440                 445
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193        Pro Ala Pro Ser Leu Leu Arg
194            450                 455
196 <210> SEQ ID NO: 3
197 <211> LENGTH: 483
198 <212> TYPE: DNA
199 <213> ORGANISM: Homo sapiens
200 <220> FEATURE:
201 <221> NAME/KEY: CDS
202 <222> LOCATION: (1)..(483)
203 <400> SEQUENCE: 3
204        gat agt gtg tgt ccc caa gga aaa tat atc cac cct caa aat aat tcg     48
205        Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser
206         1               5                  10                  15
207        att tgc tgt acc aag tgc cac aaa gga acc tac ttg tac aat gac tgt     96
208        Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys
209                    20                  25                  30
210        cca ggc ccg ggg cag gat acg gac tgc agg gag tgt gag agc ggc tcc    144
211        Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser
212                35                  40                  45
213        ttc acc gct tca gaa aac cac ctc aga cac tgc ctc agc tgc tcc aaa    192
214        Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys
215            50                  55                  60
216        tgc cga aag gaa atg ggt cag gtg gag atc tct tct tgc aca gtg gac    240
217        Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp
218         65                  70                  75                  80
219        cgg gac acc gtg tgt ggc tgc agg aag aac cag tac cgg cat tat tgg    288
220        Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr Trp
221                    85                  90                  95
222        agt gaa aac ctt ttc cag tgc ttc aat tgc agc ctc tgc ctc aat ggg    336
223        Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn Gly
224                   100                 105                 110
225        acc gtg cac ctc tcc tgc cag gag aaa cag aac acc gtg tgc acc tgc    384
226        Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr Cys
227                   115                 120                 125
228        cat gca ggt ttc ttt cta aga gaa aac gag tgt gtc tcc tgt agt aac    432
229        His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val Ser Cys Ser Asn
230                130                 135                 140
231        tgt aag aaa agc ctg gag tgc acg aag ttg tgc cta ccc cag att gag    480
232        Cys Lys Lys Ser Leu Glu Cys Thr Lys Leu Cys Leu Pro Gln Ile Glu
233        145                 150                 155                 160
234        aat                                                               483
235        Asn
237 <210> SEQ ID NO: 4
238 <211> LENGTH: 161
239 <212> TYPE: PRT
240 <213> ORGANISM: Homo sapiens
241 <400> SEQUENCE: 4
242        Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser
243         1               5                  10                  15
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 08/27/2003
PATENT APPLICATION: **US/09/899,422A**   TIME: 12:54:44

Input Set : **N:\EBONY'S\US09899422A.raw.txt**
Output Set: **N:\CRF4\08272003\I899422A.raw**

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:23; N Pos. 344,4157,5135,6255
Seq#:28; Xaa Pos. 4
Seq#:29; Xaa Pos. 7
Seq#:32; Xaa Pos. 1,2
Seq#:36; Xaa Pos. 6,10,11,12
Seq#:41; Xaa Pos. 9,10,11
Seq#:43; Xaa Pos. 6,18
Seq#:44; Xaa Pos. 16,17
Seq#:46; Xaa Pos. 7

Invalid Line Length:
The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 5

VERIFICATION SUMMARY DATE: 08/27/2003
PATENT APPLICATION: **US/09/899,422A** TIME: 12:54:44

Input Set : **N:\EBONY'S\US09899422A.raw.txt**
Output Set: **N:\CRF4\08272003\I899422A.raw**

```
L:8 M:270 C: Current Application Number differs, Wrong Format
L:1087 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23 after pos.:300
M:341 Repeated in SeqNo=23
L:1560 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28 after pos.:0
L:1576 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29 after pos.:0
L:1611 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32 after pos.:0
L:1663 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36 after pos.:0
L:1722 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:41 after pos.:0
L:1754 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43 after pos.:0
M:341 Repeated in SeqNo=43
L:1770 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44 after pos.:0
M:341 Repeated in SeqNo=44
L:1797 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46 after pos.:0
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STATISTICS SUMMARY
PATENT APPLICATION: **US/09/899,422A**

DATE: 08/27/2003
TIME: 12:54:44

Input Set : **N:\EBONY'S\US09899422A.raw.txt**
Output Set: **N:\CRF4\08272003\I899422A.raw**

Application Serial Number: US/09/899,422A
Alpha or Numeric or Xml: Numeric
Application Class:
Application File Date: 07-03-2001
Art Unit: 1600
Software Application: PatentIN2.0
Total Number of Sequences: 97
Total Nucleotides: 19901
Total Amino Acids: 3746
Number of Errors: 0
Number of Warnings: 14
Number of Corrections: 1

MESSAGE SUMMARY

270 C: 1 (Current Application Number differs)
341 W: 14 ((46) "n" or "Xaa" used)